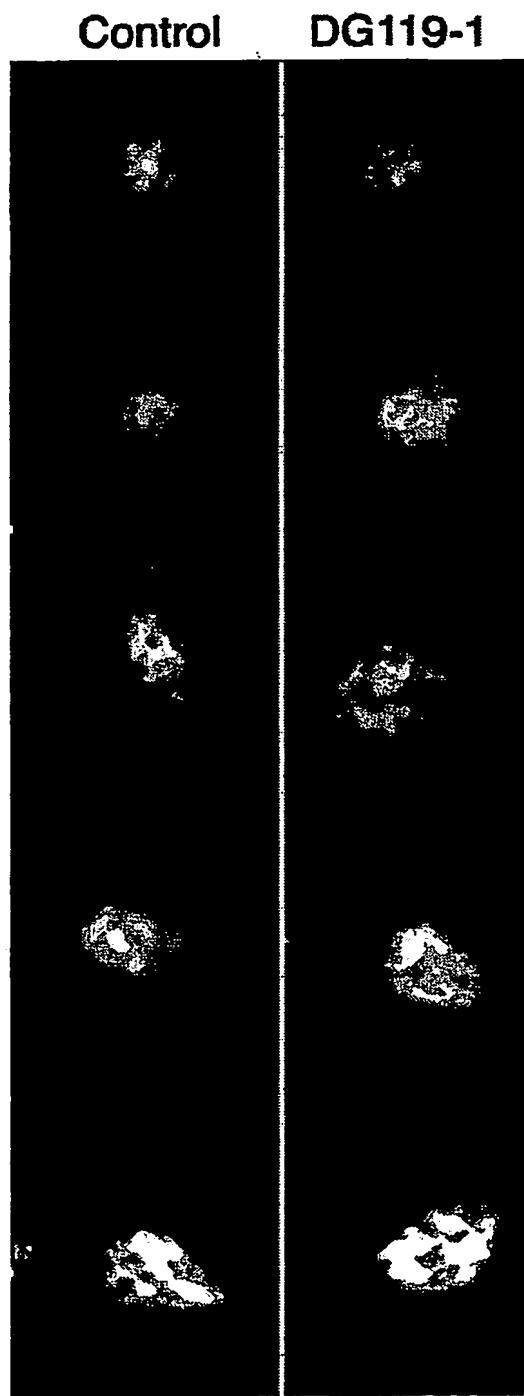


Fig. 1



**Fig. 2**

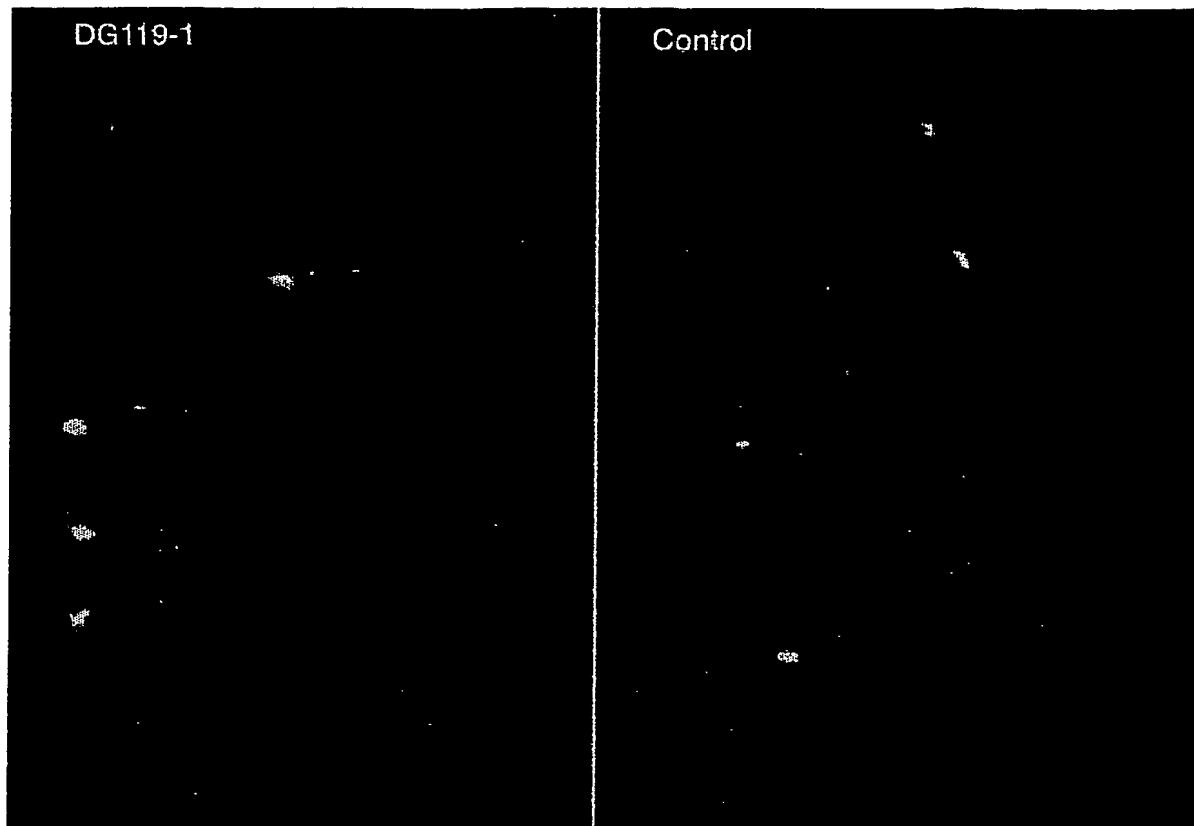


Fig. 3

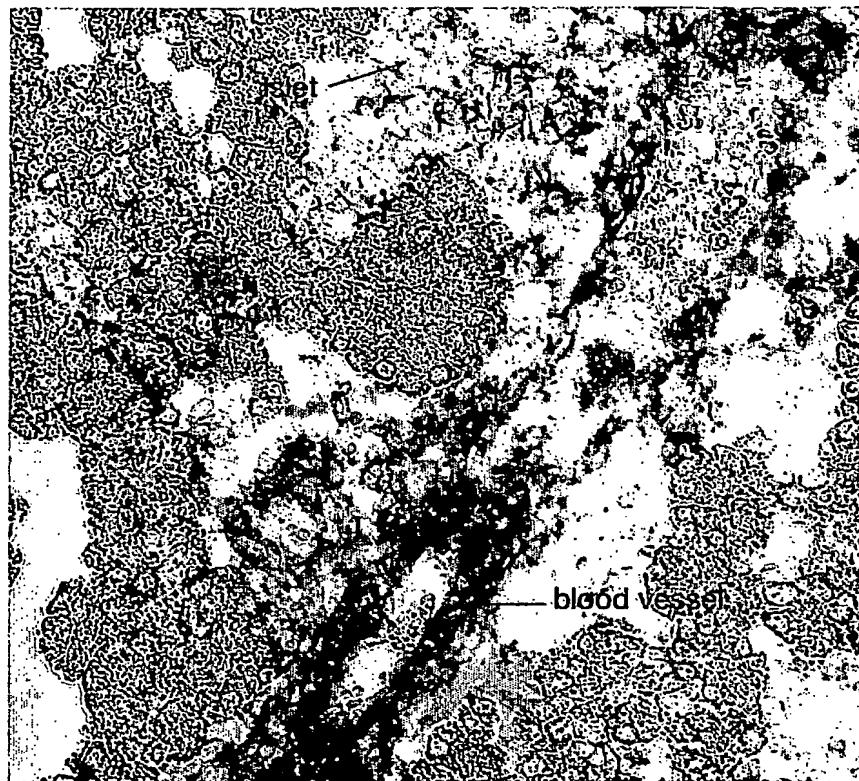


Fig. 4A

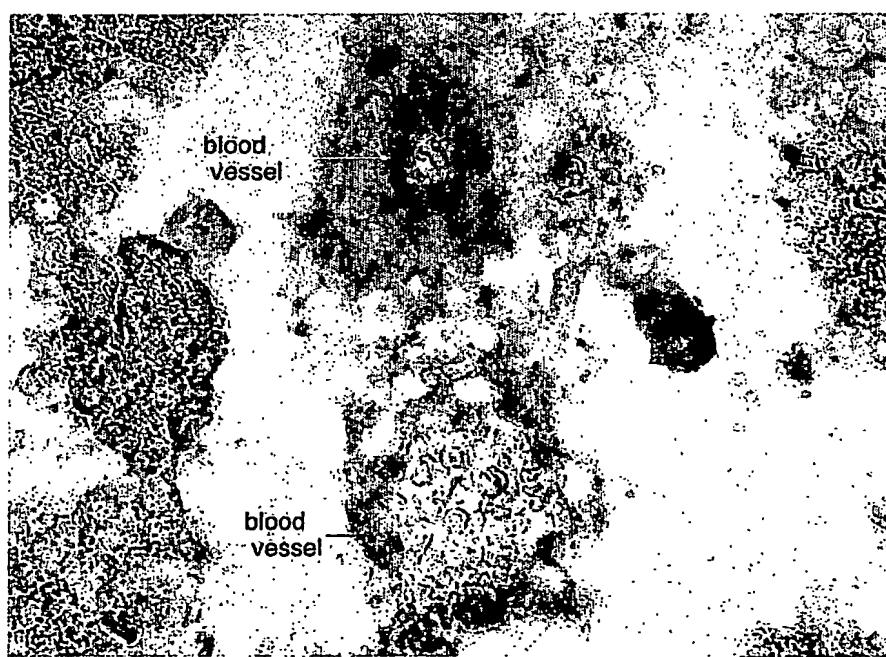


Fig. 4B

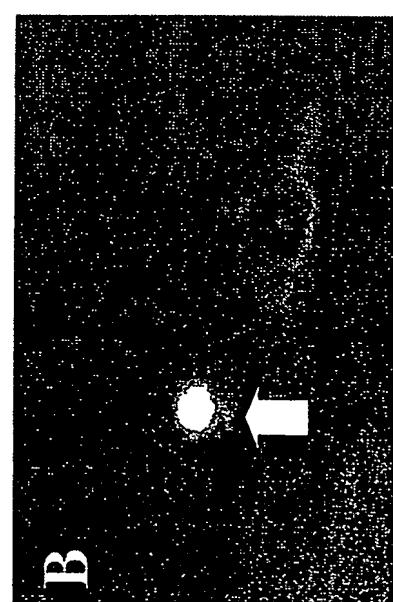
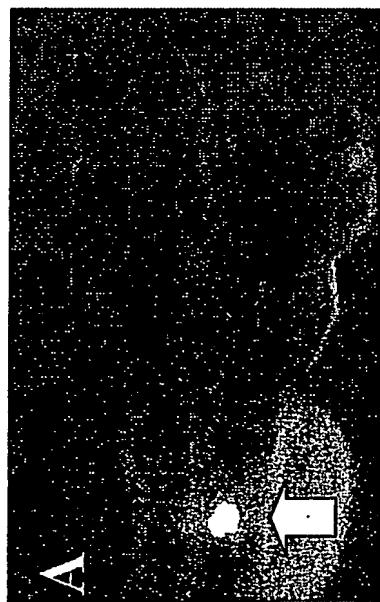
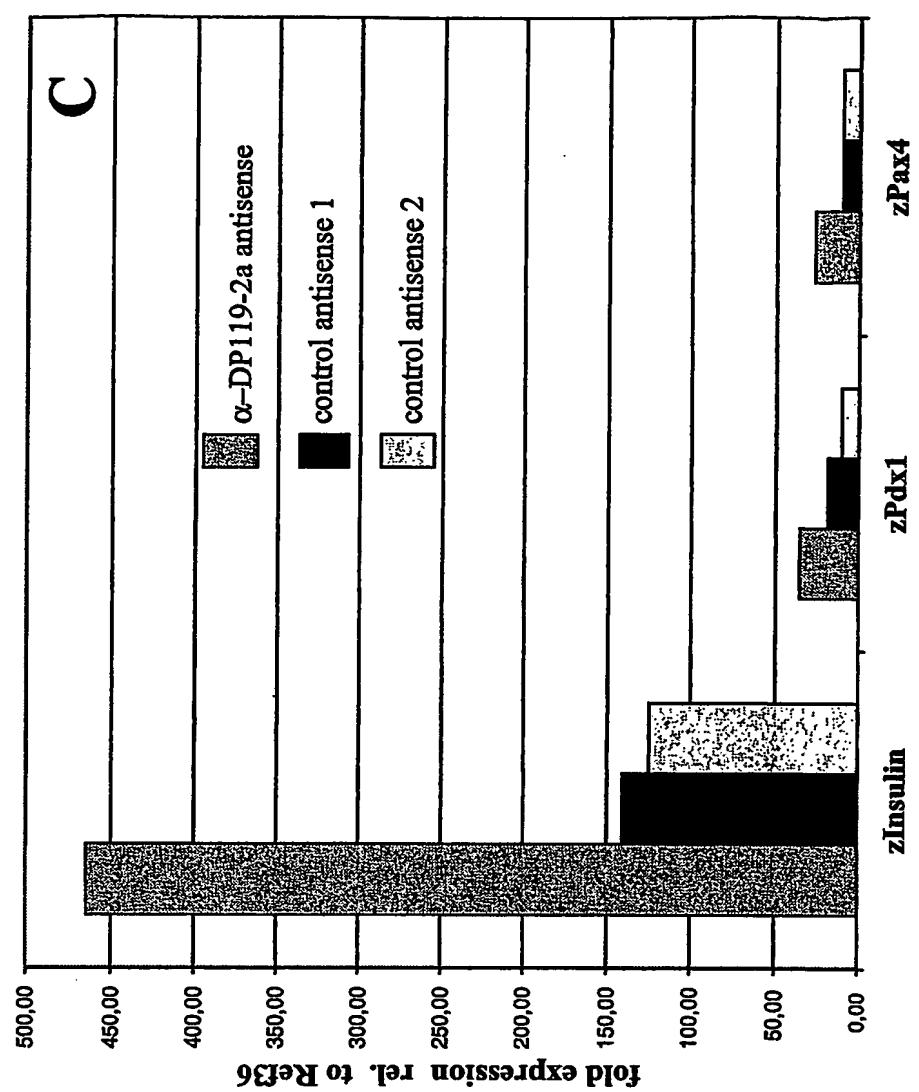


Fig. 5

1 MTEMKIWCVL LMAFALTSAA PKSHLRLEEK TKDNNDTLQV EIDNOEHILS QLLGDYDKVK  
 61 ALSEGSDCGC KCVVRPLSAS ACQRIREGHA TPQDFYTVE ITSGPHCKCA CIAPPSALNP  
 121 CEGDFRLKKL RQAGKDNIKL STILELEGS FYGMDLLKLH SVTTKILDRL DTIEKMLN  
 181 QTEEKLNNTIS TSPNPQLSTS SPPTLPSVIQ EKSTSLRQON DEAAAOFQHME SKYEKFVGD  
 241 ILNSGSDLNK ATTALQEQQ QGRKKQPKIT VRGITYYRSD PVDEMDSEKN LKETTSASSVT  
 301 QTGALIKEHL KASTQSTLNNT LTPSPTSHSN ALTVTESSVG INAHKGEVTT IVMTASVTGS  
 361 KTDSTVTLTQ LSPRVRETLT TTRTTTKTAT TSQPVKRKYS ISWDEEEEAV VPEQVEEKA  
 421 VKPVEDKVG EEPQRKPGTA HHQAKTISTV KQOIKFSLGM CKDTLATISE PITHINTYGRN  
 481 EGAWMKDPLD QDDKIVVTNY YYGNNLMLFR NIDVFKQGRF TNSYKLPYNW IGTGHVVYKG  
 541 AFYNNRAFSR DIIKFDLRLR YVAAWTMLHD AVFENDQDSS WRWRGNSDMD LAIDESGLWV  
 601 IYPALDDEGF LOEVIVLRLR NPTDLSMKRE TTWRGTLRRN RYGNCFIVCG VLYATDSYNQ  
 661 QDTNLSSYAFD THTNTQVIPH LPFSNNYTYV TQIDYNPKER VLYAWDNGHQ VTYNVQFAY

Fig. 6A

1 MGLLLWYIFCC VFCLTRANVE QOATDMDNR ATLEDEMDNQ ENILTQLIGD YDKVKTLSEG  
 61 SDCQCKCVVR PMSRSACKRI EEAQAKIEDF YTVEPVTAGP NCKKCACIAP PSALNPCEGD  
 121 FRFKKLQKKTG QYDIKLSNIM DLLEERVDNI EKGEKGQGKG ARSNORQEKK KRLSVVCWSL  
 181 HCRRTQQRLL LTLYRRCXSV LEPSLQKNAA AAAFAHTEVQM QQFIPDQRKY EEKFVGNQGP  
 241 SKPVLLKSKS EGQEEQHKPA KTKADAKMS LRSMTFYKAN RMEDSEGEER DLIIEDQLHMK  
 301 QGLNTPVTTP EATVTVTQST TINLNTQNFT TARMSNVTKQ TQGQSVKAMM SSTI TTERPT  
 361 MPTSTTSTST MTPGTNTTTI ATPLUVPKQL ASVTVGQVSN SYKLPYNWIG TGHVVYSGSF  
 421 FYNRAFSRDI IRFDLRLRYV AAWTTLHDAI LEEEAPWTW GGHSDIDFSV DESGLWLVYP  
 481 ALDDEGFHQE VIILSKLRAS DLQKEKSWRT GLRRNYYGNC FVICGVLYAV DSFERTHANI  
 541 SYAFDTHTHT QMIPRLPFIN NYTTTQIDY NPKERMLYAW DNGHQVTYDV IFAY

Fig. 6B

1 MWRIVELVAC LLMMSSHVSS QSKIFGEEQV RMTSEGSDCR CKCIMRPLTR DACARLRTGS  
 61 VRVEDFYTVE TVSSGADCKC SCTAPPSSLN PCENEWREK LKKQAPELLK LQSMVDLLEG  
 121 TLFSMDLLKV HSYINKVVSQ MNNLEE

Fig. 6C

1 MWIYASVLTY LLLLTRDARS LSKIFGEPEP VKMISEGSDC RCKCVMRPLS IEACSRRLDG  
 61 SLRVDDFYTV ETVSSGSDCK CSCTAPPSSL NPCENEWRTE KLKKQAPELL KLHSMVDLLE  
 121 GTLYSMDLMK VHAYMNKVVS QMNTLEEVMT IKTNLTRENE FVRDSVVNL NQLKRYENYS  
 181 DIMVSIKKEI SSLGLQLLQK DAASDSKAQV GTESKKSKEA IKPPNKKPPA VKPPPQKPE  
 241 KPVPKKEAP AKAAPPAKPD PTTKTKTSVH QTGVIRGITY YKASKSE

Fig. 6D

		10	20	30	40	50	60
DG119-1	Mm	-----MAYPLPLVLCFALVVAQVWGSTTPGTSEPPDVQTVPETEDDILQNEADNQEN					
DG119-1	Hs	-----MAKPRLLVLYPALIVVPAWVSSIVLTGTSEPPDAQTVAPAEDETLQNEADNQEN					
DG119-1a	Dr	-----MTEMKIWCVLLMMAFALTSAAFKS-----HLRLIEEKTKDNNDTLOVEIDNQEH					
DG119-1b	Dr	-----MGLLLYIFCCVFCLTRAN-----VEQQATDNTDNRATLEDEMDNQEN					
DG119-2a	Dr	-----MWRIVELVACLLMMSS-----HVS					
DG119-2b	Dr	-----MWIYASVLTYLLLTR-----DAR					
DG119-2	Mm	MEAAAVLPRYLQLRLLLVLLLLVLRLRAG-----PVW					
DG119-2	Hs	-----MAAAALPPRPLLPLVLLLSGR-----PTR					
----- ----- ----- ----- ----- ----- -----							
		70	80	90	100	110	120
DG119-1	Mm	VLSQLLGDYDKVKAVSEGSDCQCKCVVRPLGRDACQRINQGASRKEDFYTVETITSGSSC					
DG119-1	Hs	VLSQLLGDYDKVKAMSEGSDCQCKCVVRPLGRDACQRINAGASRKEDFYTVETITSGSSC					
DG119-1a	Dr	ILSQLLGDYDKVKALSEGSDCGCKCVVRPLSASACQRIREGHATPQDFYTVETITSGPHC					
DG119-1b	Dr	ILTQLIGDYDKVKTLSEGSDCGCKCVVRPMRSACKRIEQAQAKIEDFYTVEPVTAGPNC					
DG119-2a	Dr	SQSKIFGE-EQVRMTSEGSDCCKCIMRPLTRDACAARLRTGSVRVEDFYTVETVSSGADC					
DG119-2b	Dr	SLSKIFGEPEPVKMISEGSDCCKCIMRPLSIEACSRSLRDGSRLVDDFYTVETVSSGADC					
DG119-2	Mm	PDSKVFSDLDQVVRTSEGSDCCKCIMRPLSKDACSRSVRSGRARVEDFYTVETVSSGADC					
DG119-2	Hs	ADSKVFGDLDQVVRTSEGSDCCKCIMRPLSKDACSRSVRSGRARVEDFYTVETVSSGADC					
----- Cystein rich domain -----							
----- ----- ----- ----- ----- ----- -----							
		130	140	150	160	170	180
DG119-1	Mm	K-CACVAPPSSAVNPCEGDFRLQKLREADSRDLK-----					
DG119-1	Hs	K-CACVAPPSSALNPCEGDFRLQKLREADSPLDKVGPQCLGREGTFEIHKSGKAMVED					
DG119-1a	Dr	K-CACIAPPSSALNPCEGDFRLKQLRQACKDNK-----					
DG119-1b	Dr	KKCACIAPPSSALNPCEGDFRFKKLQKTTGQYDIK-----					
DG119-2a	Dr	K-CSCTAPPSSLNPCENEWKRKEKKQAPEELLKLQ-----					
DG119-2b	Dr	K-CSCTAPPSSLNPCENEWRTKLKKQAPEELLKLH-----					
DG119-2	Mm	R-CSCTAPPSSLNPCENEWKMEEKKQAPEELLKLQ-----					
DG119-2	Hs	R-CSCTAPPSSLNPCENEWKMEEKKQAPEELLKKS-----					
----- Cystein rich domain -----							
----- ----- ----- ----- ----- ----- -----							
		190	200	210	220	230	240
DG119-1	Mm	-----LSTIID					
DG119-1	Hs	SKPFEEGLSHFLTQTFRKAECTTYTIVLAYIPVYTNVFLTATSQFLASGFPVEPPLSTIID					
DG119-1a	Dr	-----LSTIIE					
DG119-1b	Dr	-----LSNIMD					
DG119-2a	Dr	-----SMVD					
DG119-2b	Dr	-----SMVD					
DG119-2	Mm	-----SMVD					
DG119-2	Hs	-----					
----- ----- ----- ----- ----- ----- -----							
		250	260	270	280	290	300
DG119-1	Mm	MLEGAFYGLDLLKLHSVTTKLVG-----RVDKLEE					
DG119-1	Hs	MLEGAFYGLDLLKLHSVTTKLVGRVDKLEEMLEGAFYGLDLLKLHSVTTKLVGRVDKLEE					
DG119-1a	Dr	LLEGSTFYGM DLLKLHSVTTKILD-----RMDTIEK					
DG119-1b	Dr	LLEGSTFYGM DLLKLHSVTTKLL-----RVDNIEK					
DG119-2a	Dr	LLEGTLFSMD DLLK VHSYINKVVS-----QMNLEE					
DG119-2b	Dr	LLEGTLYSMD DLLK VHAYMNKVV-----QMNLEE					
DG119-2	Mm	LLEGALYSMD DLLK VHAYIQKVAS-----QMNLEE					
DG119-2	Hs	-----					
----- ----- ----- ----- ----- ----- -----							
		310	320	330	340	350	360
DG119-1	Mm	E--VSKNLTKENEQIKEDVEEIRTELN-KRGKENCSDNTLESMPDIRSALQRDAAA-----					
DG119-1	Hs	E--VSKNLTKENEQIKEDMEEIRTEMN-KRGKENCSENILDSDMPDIRSALQRDAAA-----					
DG119-1a	Dr	M--VLNQTEEKLNNTISTSPNP-----QLSTSS-----PTTLPSPVIEQEKST-----					
DG119-1b	Dr	S--FSGNLITKEKVSVKGEGKGQG-----KGARSNQRQEKKRSLVLEPSLQKNAAA-----					
DG119-2a	Dr	-----					
DG119-2b	Dr	VMTIKTNL TRENEFVRD SVVNLSNQLKRYENYSDIMVS IKKEISSLGLQLLQKDAA-----					
DG119-2	Mm	S--IKANL SLENKVV KDSVHHLSEQLKSYENQSAIMMSIKKELSSIGLQLLQRDAAA VPA					
DG119-2	Hs	---IKANL SRENEVV KDSVHLSEQLRHYENHS AIMLG IKKEL SRLGLQLLQKDAAA VPA					

Fig. 7

		370	380	390	400	410	420
DG119-1	Mm	-----AYAHP--EYEERFLQEETVSQQINSIELLRTQPLVPPAAMKPQRFLQRQVHL					
DG119-1	Hs	-----AYAHP--EYEERFLQEETVSQQINSIELLQTRPLALPEVVKSRPLQRQVHL					
DG119-1a	Dr	-----SLRQON-DEAAAFQHMESEKYEEKFVGDIILNSGSDLNKATTALQE--OEOOGR					
DG119-1b	Dr	-----AFAHTE-VQMQQFI PDQRKYEEKFVGQNQGPKVPLKKSKSEGQE--EQHKPA					
DG119-2a	Dr	-----					
DG119-2b	Dr	-----SDSKAQVGTESKKSKSEA1KPPNKKPPAVKPPPKQPKVVKPKKEAPAKAAKPA					
DG119-2	Mm	-----TAPASSPDSKAQDTAGGQGRDLNKYGSIQKSFSDKGLAKPPKEKLLKVEKLR-KESIKGR					
DG119-2	Hs	-----TPATG-TGSKAQDTARGKGKD1SKYGSVQKSFDARGLPKPKKEKLLQVEKLR-KESGKGS					
		430	440	450	460	470	480
DG119-1	Mm	-----RGRLASK-----PTVIRGITYYKAKVSEEENDIEQHDELFSGDGVLDLIEDQLLRQ					
DG119-1	Hs	-----RGRPASQ-----PTVIRGITYYKAKVSEEENDIEQHDEFFSGDNGVLDLIEDQLLRQ					
DG119-1a	Dr	-----KKQP-----KTVRGITYYRSDPVDEMDSEKLNKETSASSVTQTCGALIKEHLKAS					
DG119-1b	Dr	-----KTKADAK-----NMSLRSMTFYKANRMEDSEGEE-----RMDLIIEDQLHKQ					
DG119-2a	Dr	-----					
DG119-2b	Dr	-----KPDPTTKTKTSVHQTGVIRGITYYKAGR-----					
DG119-2	Mm	-----IPQPTARPRALAQQAVIRGFTYYKAGRQEARQEAPKAAADSTLKGTSWLEKLPK					
DG119-2	Hs	-----FLQPTAKPRALAQQAVIRGFTYYKAGRQE-----VTEAVADNALQGTTSWLEQLPPK					
		490	500	510	520	530	540
DG119-1	Mm	-----ED--LLTSATRRPATR-----HTAAVITDASIQAASSSEPAQASASASSFVEPAPQASDRE					
DG119-1	Hs	-----NG--LMTSVTRRPAATRQGHSTAVTSDLNARTAFWSSALPQPSTSDPSIANHASVGP-----					
DG119-1a	Dr	-----TQSTLNTLTPSPSTSNSALTVTESSVGINAHGEVTTIVMTASVTGSKTDVTSVDTLQLSP					
DG119-1b	Dr	-----G--LNTPVTTPEAT-----VTVTQSTT--INLNTQNFTTARMNSVTKQTQGQSVKAMMSS-----					
DG119-2a	Dr	-----					
DG119-2b	Dr	-----					
DG119-2	Mm	-----IEAK--LPEPNSAKHDDVRLQAEGGNLTPDITTTTTSTSSTSSTTTTGTTSTTSTTSTTS					
DG119-2	Hs	-----VEGRNSNAEPNSAEQDEAEPRS SERVDLASFSTHLLPPLHSLHHHSTPVLATPAPFHLOC					
		550	560	570	580	590	600
DG119-1	Mm	-----LLATPQTTVFPEPTG-----VMPSTQVSPPTVAHTAVQP-----LPAMVPGDIFVEALPLV					
DG119-1	Hs	-----TQTTSVSPDPTRESVLOQSPQVPATTVAHTATQQPAAPAPPFAVSPREALMEAMHTV					
DG119-1a	Dr	-----RVRETLTTTRTTTKTA-----TTSQPVKRKYSISWDEEEE-----AVVP-EQVEEKAVK					
DG119-1b	Dr	-----TITTERPTMPTS-----TTSTSTMTPGTNTTTIATP-----LVVP-KQLAR-----					
DG119-2a	Dr	-----					
DG119-2b	Dr	-----					
DG119-2	Mm	-----TTTPSP-----					
DG119-2	Hs	-----HNKPVPSPRRWQTPSRALPGWSNCRPRWRAQPTPQSPTQSRMRLSPGPPSEWTLLAP					
		610	620	630	640	650	660
DG119-1	Mm	-----PLLPDTVGTDMPEEEGTAGQEATSAGPILSPEEEEDDIRNVIG-----					
DG119-1	Hs	-----FVPPPTVVRTDSLGDAPAGWGTTPASPTLSPPEEEEDDIRNVIG-----					
DG119-1a	Dr	-----PVVEDKVGEEPQRKPGTAHHQAKT1STVKQOIKFSLG-----					
DG119-1b	Dr	-----					
DG119-2a	Dr	-----					
DG119-2b	Dr	-----					
DG119-2	Mm	-----ITTPWPTEPPLHPEVPSQGRED-----					
DG119-2	Hs	-----HFNPCHHHHRHPHPQPPPTSSLTEPPSGPEVSSQGRE-----					
		670	680	690	700	710	720
		730	740	750	760	770	780
DG119-1	Mm	-----RCKDTLSTITGPTTQNTYGRNEGAWMKDPLAKDRIYVTNYYYGNTLVEFRNLEN					
DG119-1	Hs	-----RCKDTLSTITGPTTQNTYGRNEGAWMKDPLAKDRIYVTNYYYGNTLVEFRNLEN					
DG119-1a	Dr	-----MCKDTLATICEPITHNTYGRNEGAWMKDPLDQDDK1YVTNYYYGNNLLEFRNLDV					
DG119-1b	Dr	-----ICKDTLASISDPVTHNKYKGNEGAWMKDPKGNGKVYVTDYYYYGNQLLEFRDIDT					
DG119-2a	Dr	-----					
DG119-2b	Dr	-----					
DG119-2	Mm	-----SCEGTLRAVDPPVKHHHSYGRHEGAWMKDPAALDDR1YVTNYYYGNSLVEFRNLEN					
DG119-2	Hs	-----SCEGTLRAVDPPVRHHHSYGRHEGAWMKDPAARDRIYVTNYYYGNSLVEFRNLEN					

Fig. 7 (cont.)

| ----- Olfactomedin-like domain -----

9/19

		790	800	810	820	830	840	
DG119-1	Mm	FKQGRWSNSYKLPYSWIGTGHVVYNGAFYYNRAFTRNIKYDLKQRYVAAWAMLHDVAYE						
DG119-1	Hs	FKQGRWSNSYKLPYSWIGTGHVVYNGAFYYNRAFTRNIKYDLKQRYVAAWAMLHDVAYE						
DG119-1a	Dr	FKQGRFTNSYKLPYNWIGTGHVVYKGAFYNNRAFSDRIKYDLRRLRYVAAWTMLHDAILE						
DG119-1b	Dr	FKQGQVSNSYKLPYNWIGTGHVVYSGSFFYNRAFSDRIKYDLRRLRYVAAWTMLHDAILE						
DG119-2a	Dr							
DG119-2b	Dr							
DG119-2	Mm	FKQGRWSNSMYKLPYNWIGTGHVVYQGAFYYNRAFTKNIKYDLRQRFVASWALLPDVVYE						
DG119-2	Hs	FKQGRWSNSMYKLPYNWIGTGHVVYQGAFYYNRAFTKNIKYDLRQRFVASWALLPDVVYE						
		olfactomedin-like domain						
		850	860	870	880	890	900	
DG119-1	Mm	--EATPWRWQGHSDVDFAVDENGLWLIYPALDD--EGFNQEIVI VLSKLNADLSTOKETTW						
DG119-1	Hs	--EATPWRWQGHSDVDFAVDENGLWLIYPALDD--EGFSQEIVI VLSKLNADLSTOKETTW						
DG119-1a	Dr	NDVSSWRWRGNSDMDLAIDESGLWVIYPALEDD--EGFLQEIVI VLSRIMPTDLSMKRETTW						
DG119-1b	Dr	-EEEAPWTWGGHSIDF SVDESGLWL VYPALDD--EGFHQEIVI ILSKL RASDL--QKEKSW						
DG119-2a	Dr							
DG119-2b	Dr							
DG119-2	Mm	--DTTPWKWRGHSDIDFAVDESGLWVIYPAVDEHDETQHEVIVLSRLDPADLSVHRETTW						
DG119-2	Hs	--DTTPWKWRGHSDIDFAVDESGLWVIYPAVDDRDEAQPEVIVLSRLDPGDL SVHRETTW						
		olfactomedin-like domain						
		910	920	930	940	950	960	
DG119-1	Mm	RTGLRRNRYGNCFVICGVL YAVDSDYNQRNANISYAFDTHTNTQIVPRLLFENEYSYTTQI						
DG119-1	Hs	RTGLRRNRYGNCFVICGVL YAVDSDYNQRNANISYAFDTHTNTQIVPRLLFENEYSYTTQI						
DG119-1a	Dr	RTGLRRNRYGNCFVICGVL YATDSYNQDNTLNSYAFDTHTNTQIVPRLPFNSNNYTYVTQI						
DG119-1b	Dr	RTGLRRNRYGNCFVICGVL YAVDSFERTHANISYAFDTHTHTQMI PRLPFINNNYTYTTQI						
DG119-2a	Dr							
DG119-2b	Dr							
DG119-2	Mm	KTRLRRNSYGNCFLVCGILYTVDTYNQHEGQVAYAFDTHTGTD AHPQLPFLNEYSYTTQV						
DG119-2	Hs	KTRLRRNSYGNCFLVCGILYAVDTYNQQEGQVAYAFDTHTGTD ARPQLPFLNEHAYTTQI						
		olfactomedin-like domain						
		970	980	990	1000	1010	1020	
DG119-1	Mm	DYNPKDRLLYAWDNGHQVTVYHVIFAY						
DG119-1	Hs	DYNPKDRLLYAWDNGHQVTVYHVIFAY						
DG119-1a	Dr	DYNPKERVLYAWDNGHQVTVNVQFAY						
DG119-1b	Dr	DYNPKERMLYAWDNGHQVTVDVIF--						
DG119-2a	Dr							
DG119-2b	Dr							
DG119-2	Mm	DYNPKERVLYAWDNGHQQLTYTLHFVV						
DG119-2	Hs	DYNPKERVLYAWDNGHQQLTYTLHFVV						
		olfactomedin-like domain						

Fig. 7 (cont.)

**rIP-*mDG119-1* tg mice**

0.8kb rat insulin II promoter

*mDG119-1*

2.2 kb

hybrid  
intron

bgh-polyA

**Fig. 8A****Pdx1-*mDG119-1* tg mice**

4.3kb mouse Pdx1-promoter

*mDG119-1*

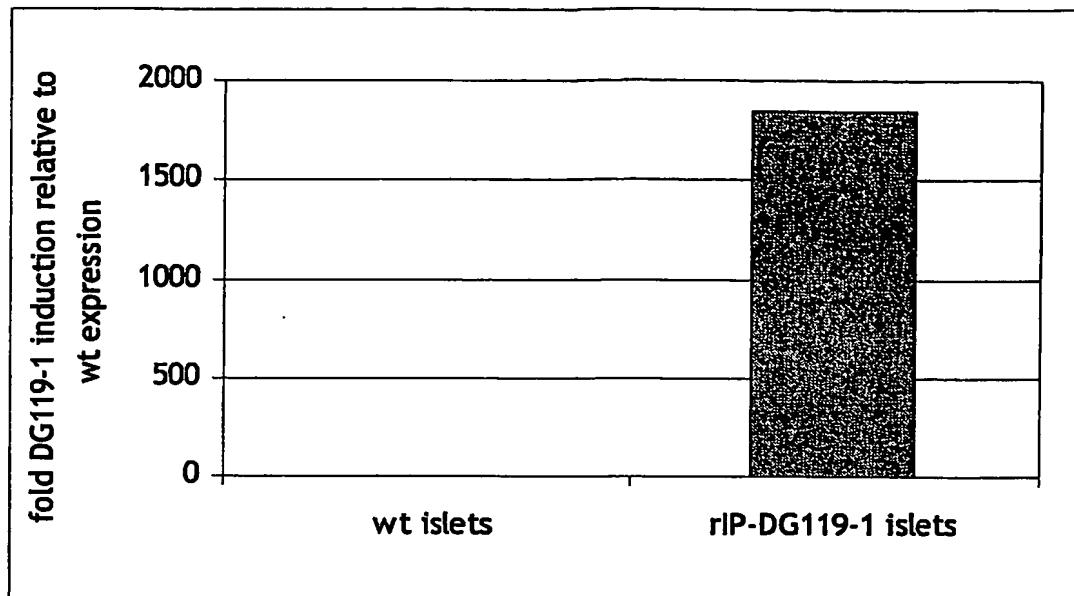
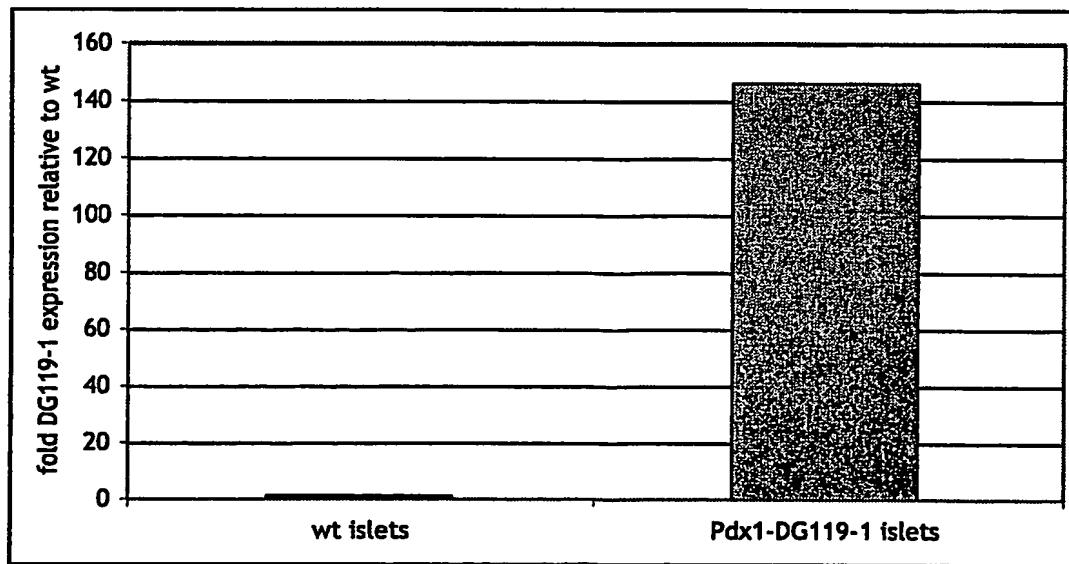
2.2kb

hybrid  
intron

bgh-polyA

**Fig. 8B**

11/19

**Fig. 9A****Fig. 9B**

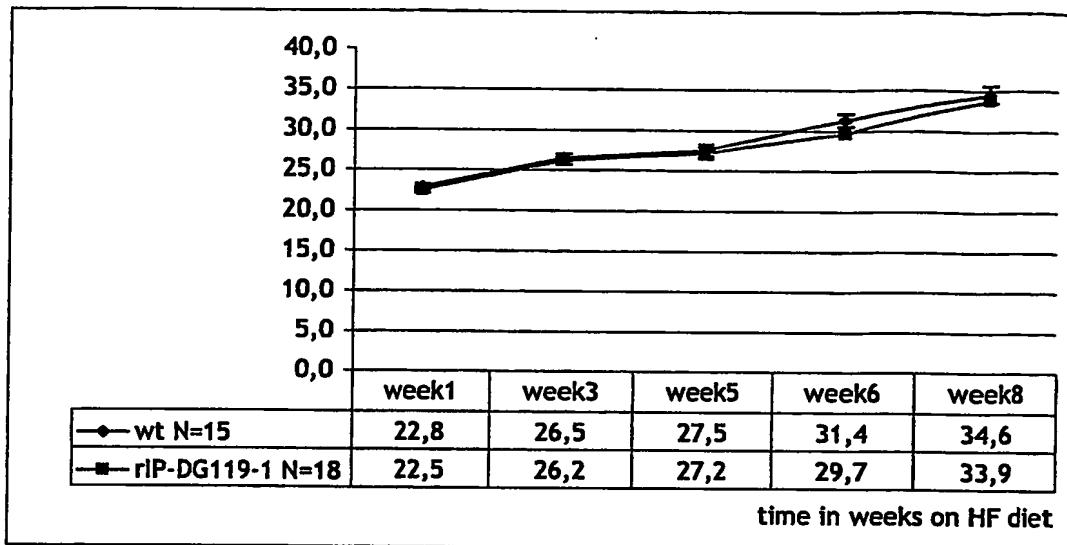


Fig. 10A

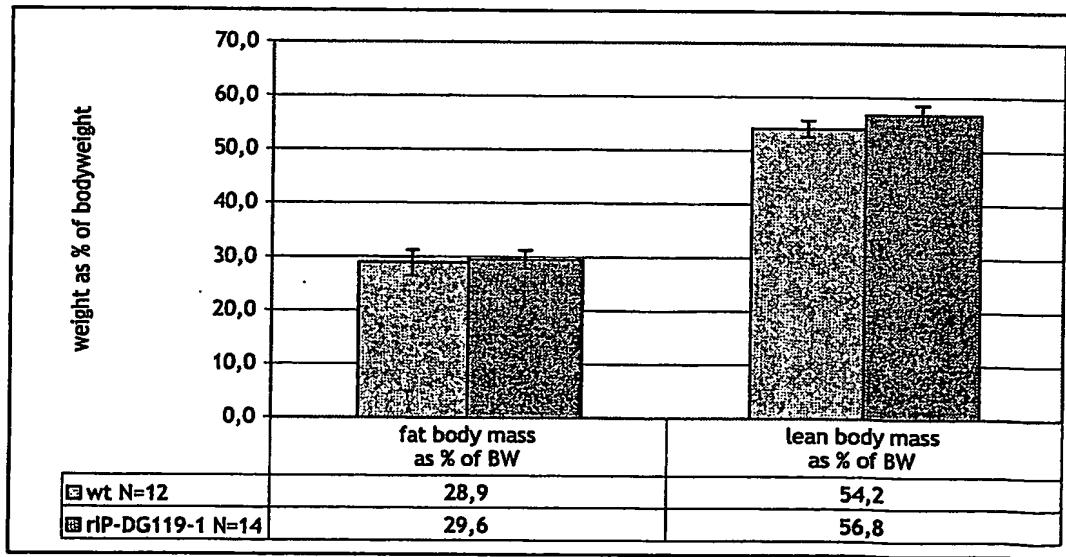


Fig. 10B

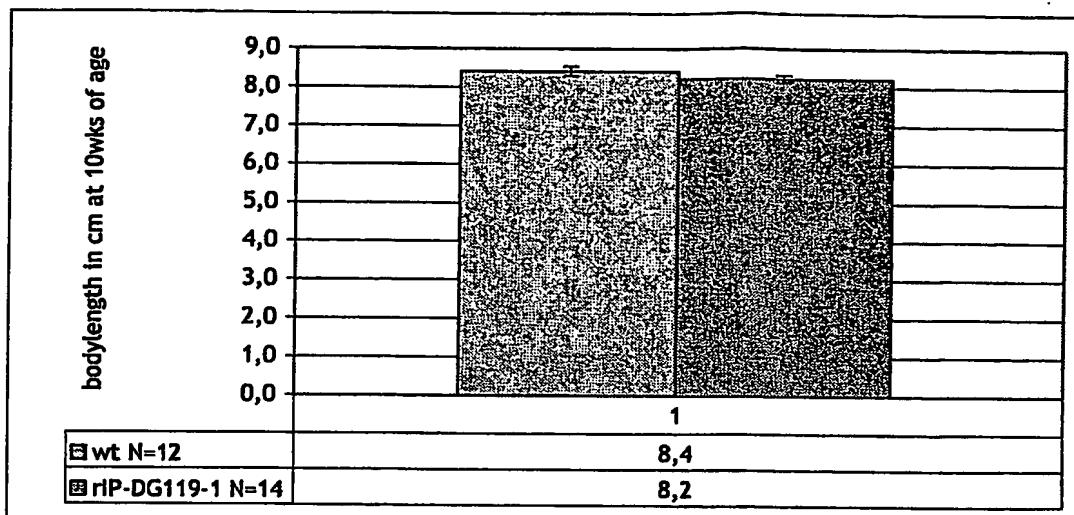


Fig. 11

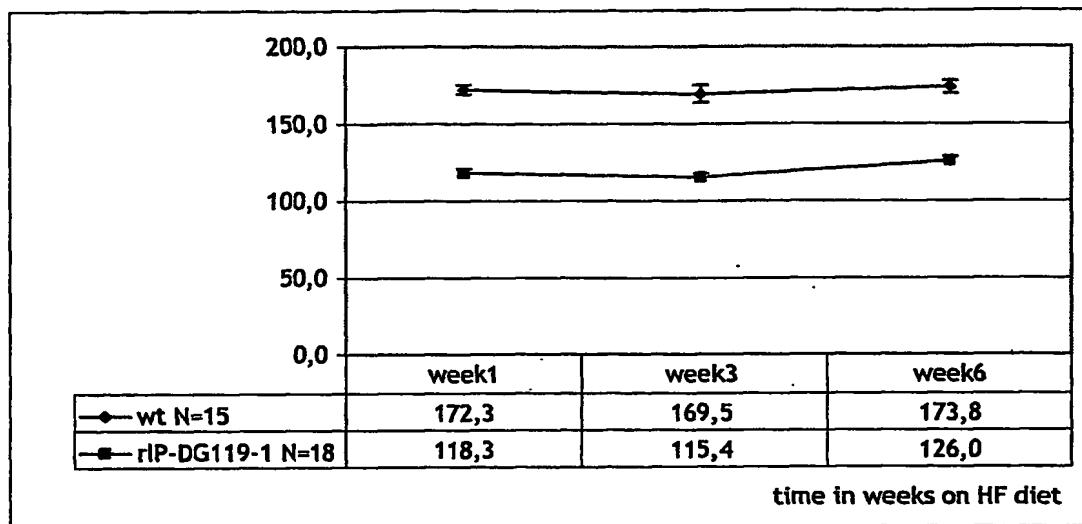


Fig. 12A

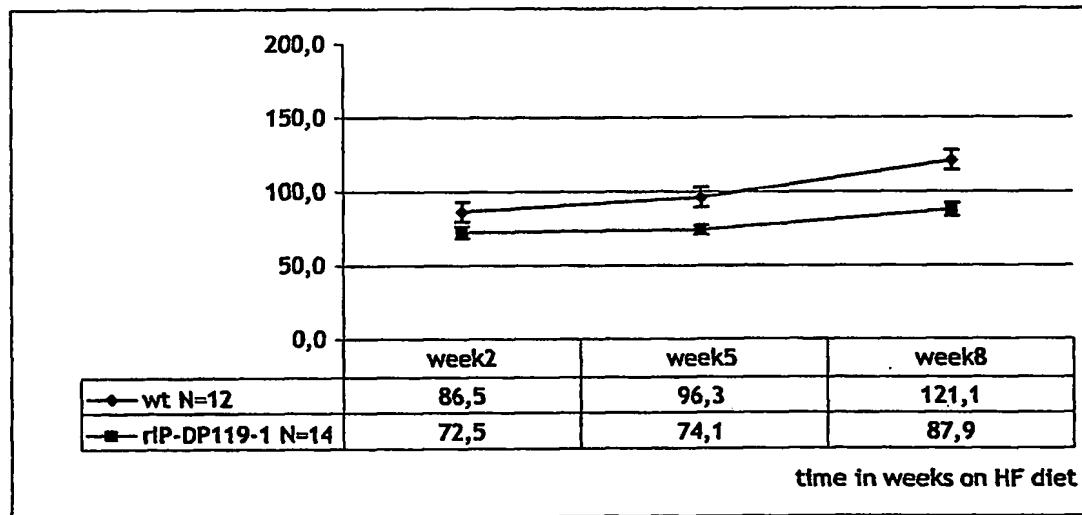


Fig. 12B

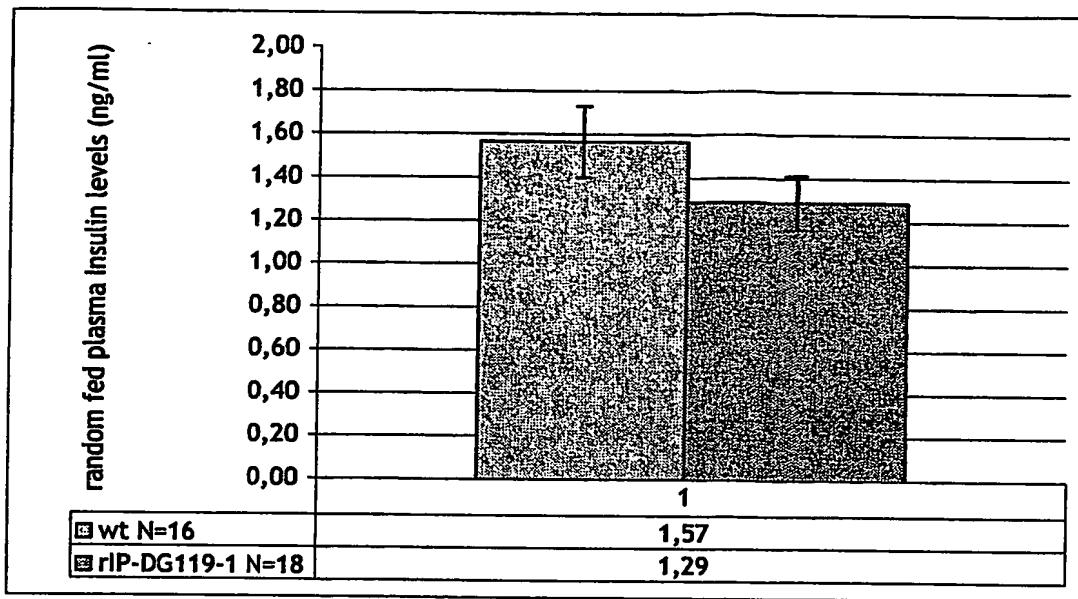


Fig. 13A

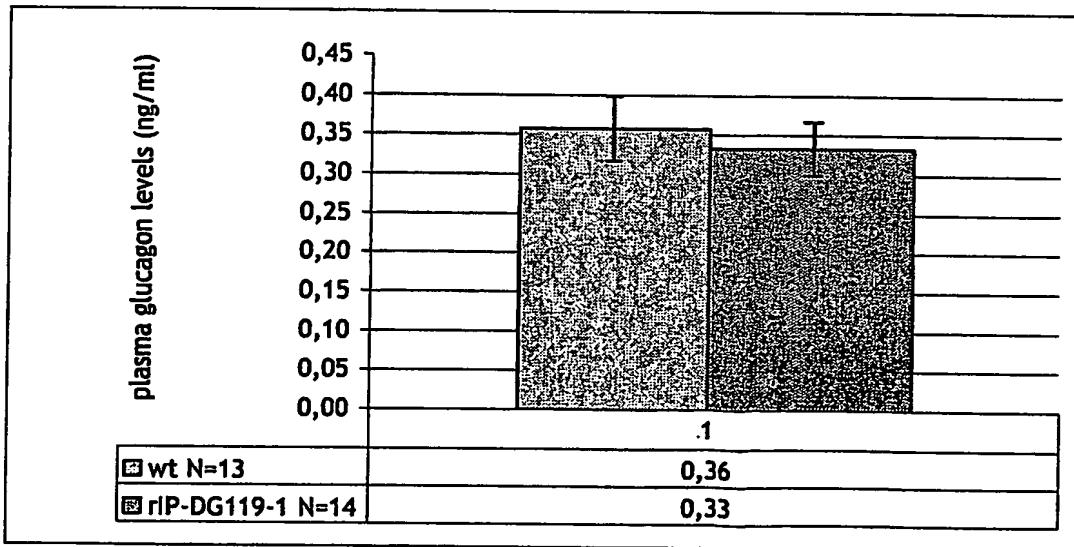


Fig. 13B

16/19

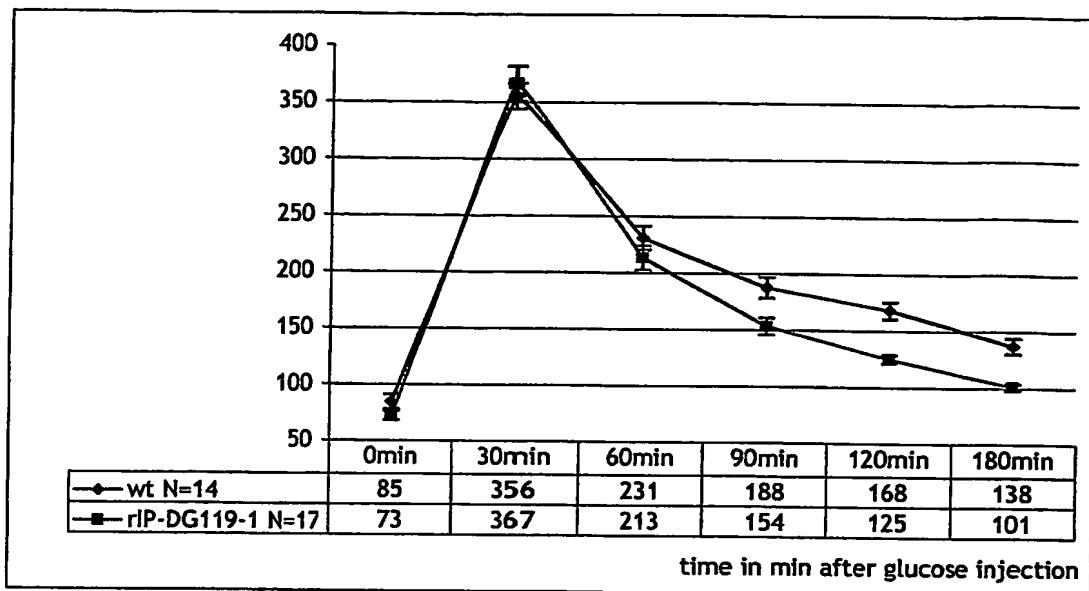


Fig. 14A

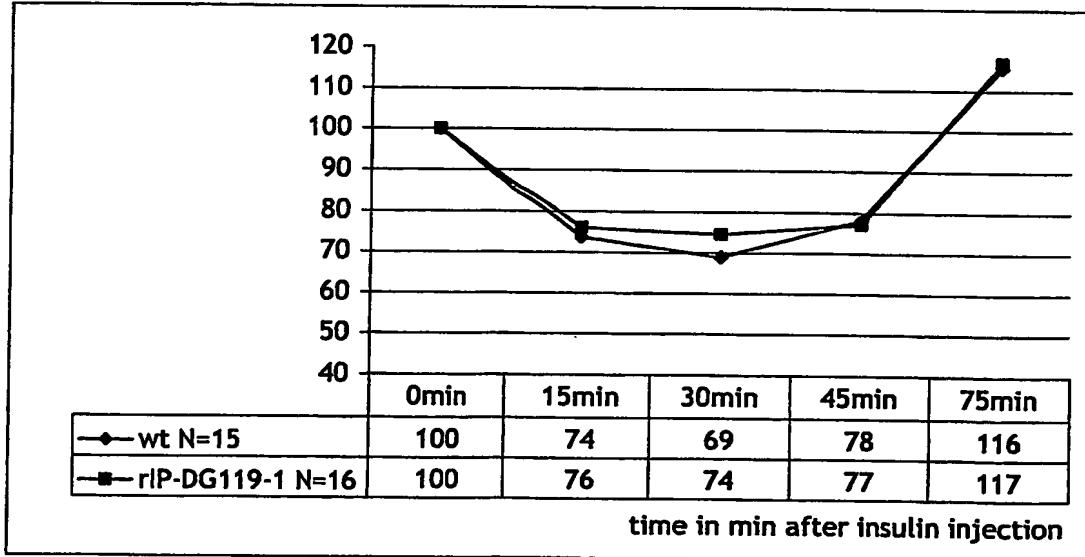


Fig. 14B

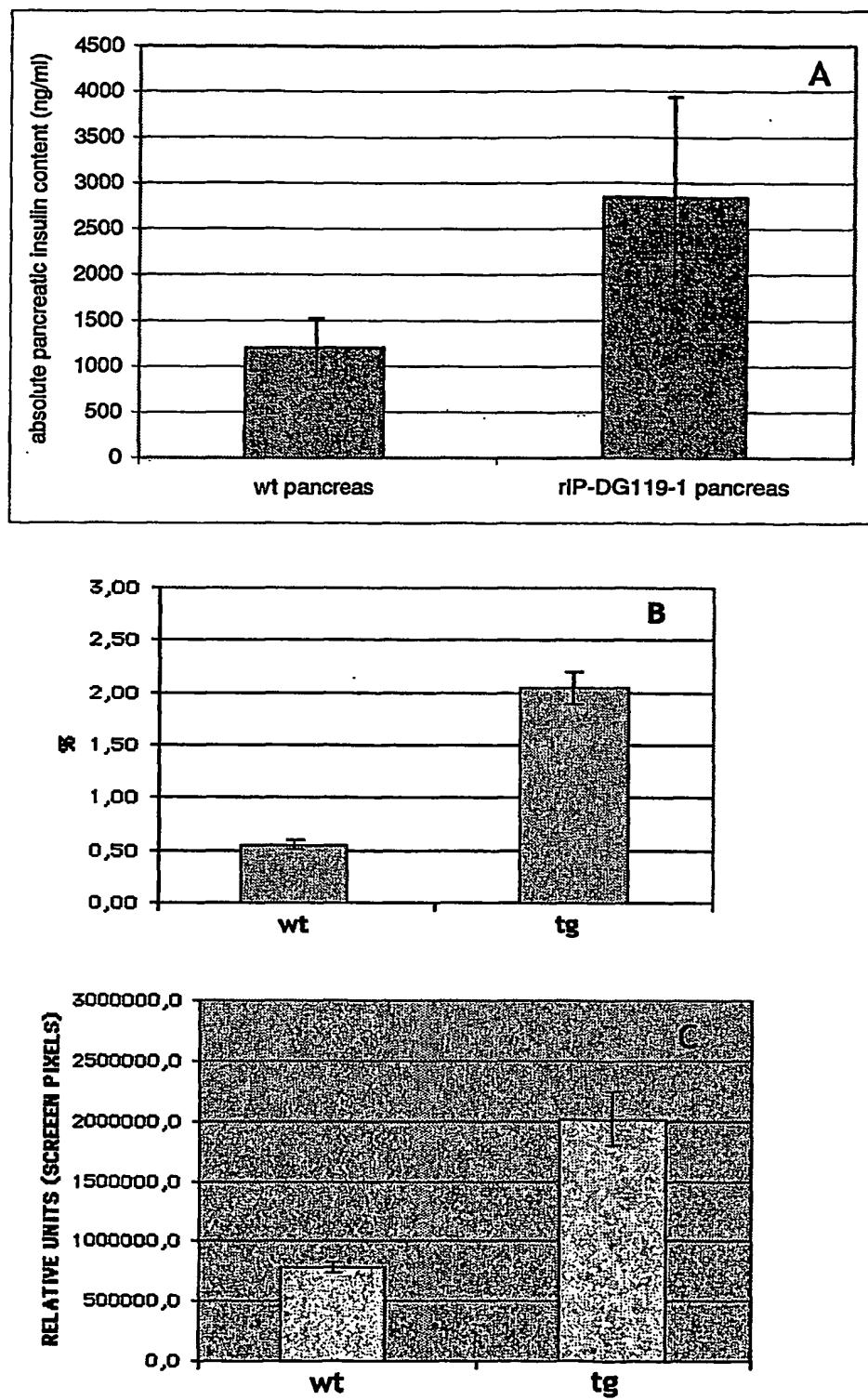


Fig. 15

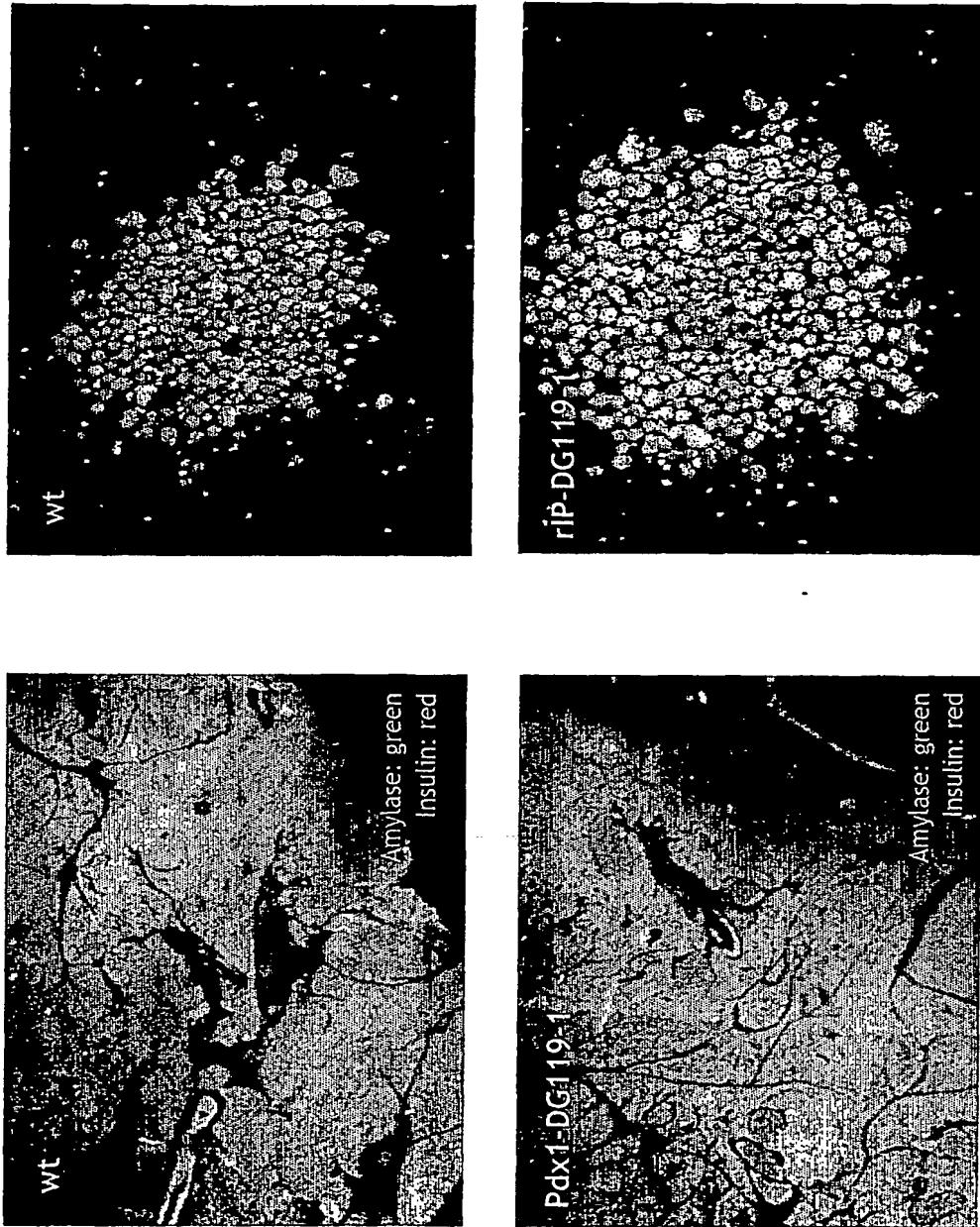


Fig. 16

19/19

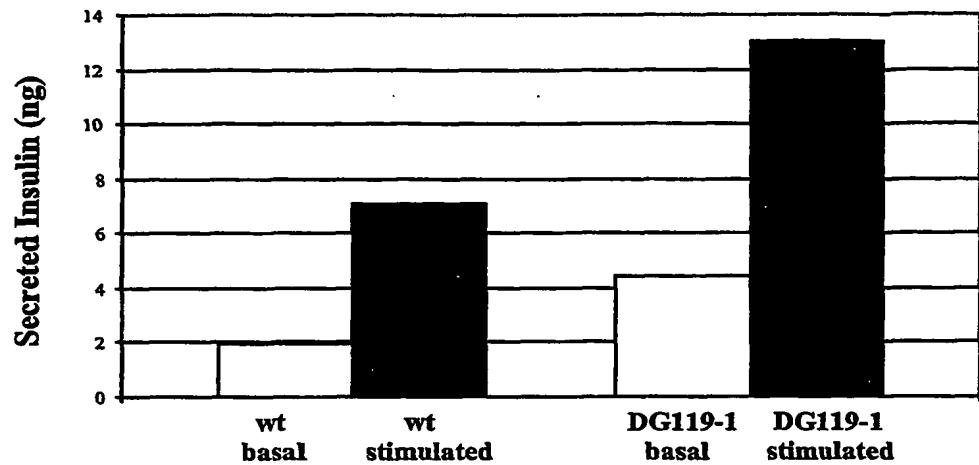


Fig. 17